Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/27 02:12:05

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam ERR2094124.sorted.bam -c -nw 400 -hm 3
```

1.2. Alignment

Command line:	/home/luna/Desktop/Software/bwa/bwa mem -t 16 -k 30 -R @RG\tID:Singlecell2022\tLB:Library\tPL:ILLUMINA\tSM:sample_ERR2094124 /home/luna/Desktop/database/homo_bwa/hsa.fa ERR2094124_1.fastq.gz ERR2094124_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Aug 27 02:12:04 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	ERR2094124.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	511,912
Mapped reads	490,131 / 95.75%
Unmapped reads	21,781 / 4.25%
Mapped paired reads	490,131 / 95.75%
Mapped reads, first in pair	245,964 / 48.05%
Mapped reads, second in pair	244,167 / 47.7%
Mapped reads, both in pair	487,408 / 95.21%
Mapped reads, singletons	2,723 / 0.53%
Secondary alignments	0
Supplementary alignments	3,847 / 0.75%
Read min/max/mean length	30 / 151 / 147.32
Duplicated reads (estimated)	491,141 / 95.94%
Duplication rate	49.88%
Clipped reads	64,650 / 12.63%

2.2. ACGT Content

Number/percentage of A's	19,994,937 / 27.54%
Number/percentage of C's	15,322,914 / 21.1%
Number/percentage of T's	21,037,342 / 28.97%
Number/percentage of G's	16,250,103 / 22.38%
Number/percentage of N's	769 / 0%

GC Percentage	43.49%

2.3. Coverage

Mean	0.0235
Standard Deviation	42.3556

2.4. Mapping Quality

Mean Mapping Quality	11.65

2.5. Insert size

Mean	7,388.9
Standard Deviation	574,440.59
P25/Median/P75	217 / 233 / 266

2.6. Mismatches and indels

General error rate	1.66%
Mismatches	1,166,174
Insertions	26,659
Mapped reads with at least one insertion	5.38%
Deletions	52,528
Mapped reads with at least one deletion	10.49%
Homopolymer indels	65.29%

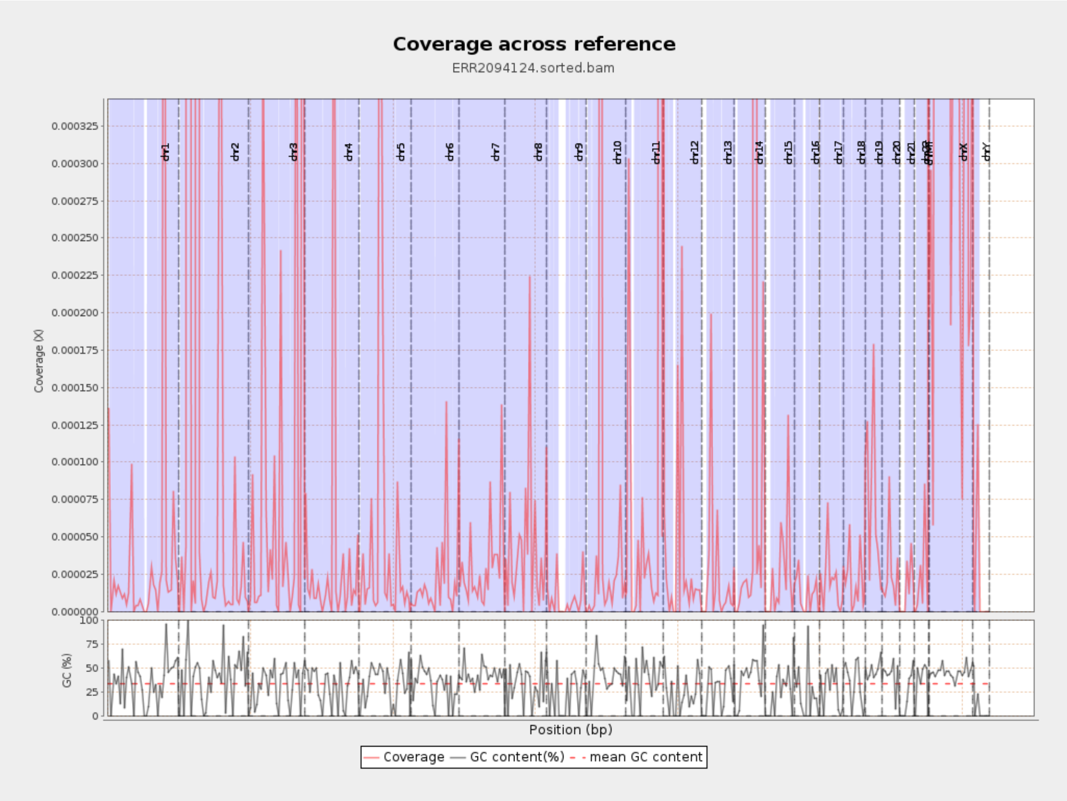
2.7. Chromosome stats

Name	**Length**	**Mapped**	**Mean**	**Standard**

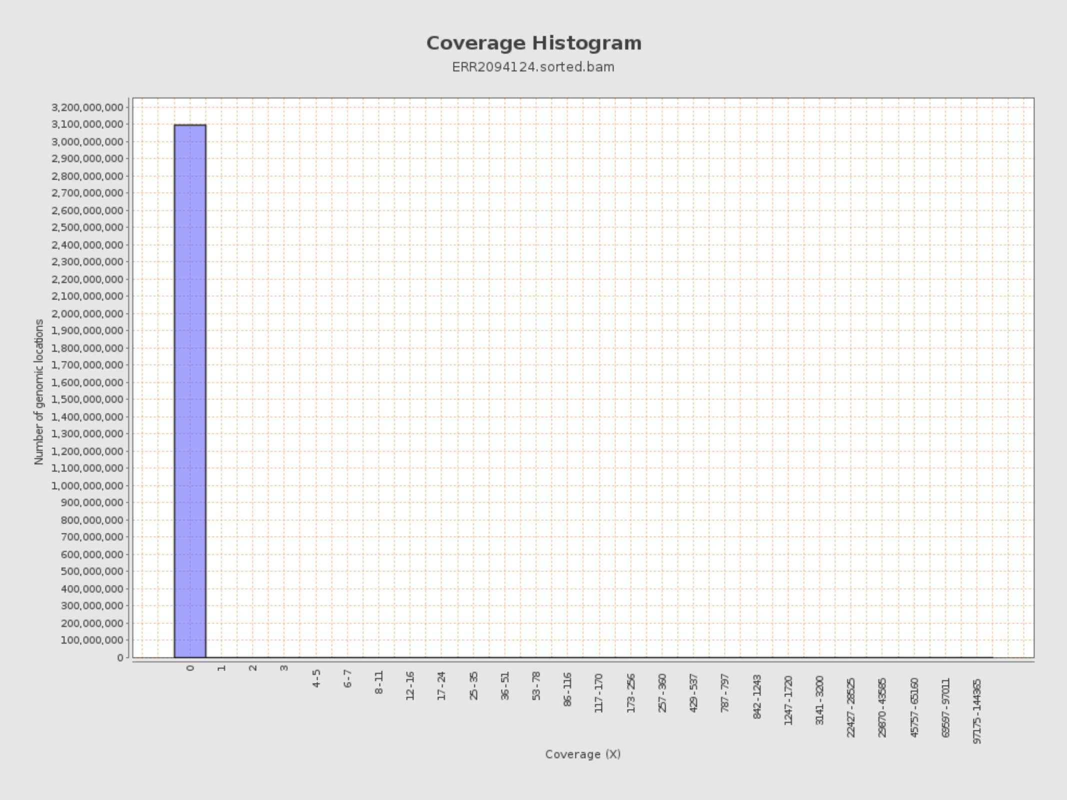
		bases	coverage	deviation
chr1	249250621	10915	0	0.0253
chr2	243199373	706434	0.0029	2.4545
chr3	198022430	19648	0.0001	0.0623
chr4	191154276	8031	0	0.0192
chr5	180915260	9342	0.0001	0.0375
chr6	171115067	3478	0	0.0085
chr7	159138663	4992	0	0.0096
chr8	146364022	6212	0	0.0139
chr9	141213431	1183	0	0.004
chr10	135534747	11392	0.0001	0.0342
chr11	135006516	49582	0.0004	0.6498
chr12	133851895	4767	0	0.0189
chr13	115169878	2881	0	0.0119
chr14	107349540	108285	0.001	1.1666
chr15	102531392	2512	0	0.0095
chr16	90354753	1124	0	0.005
chr17	81195210	1722	0	0.0059
chr18	78077248	1597	0	0.0057
chr19	59128983	4441	0.0001	0.0259
chr20	63025520	1626	0	0.0057
chr21	48129895	803	0	0.0057
chr22	51304566	1141	0	0.0066
chrMT	16571	71373080	4,307.1076	17,790.432
chrX	155270560	331832	0.0021	1.5244

chrY	59373566	1041	0	0.0093

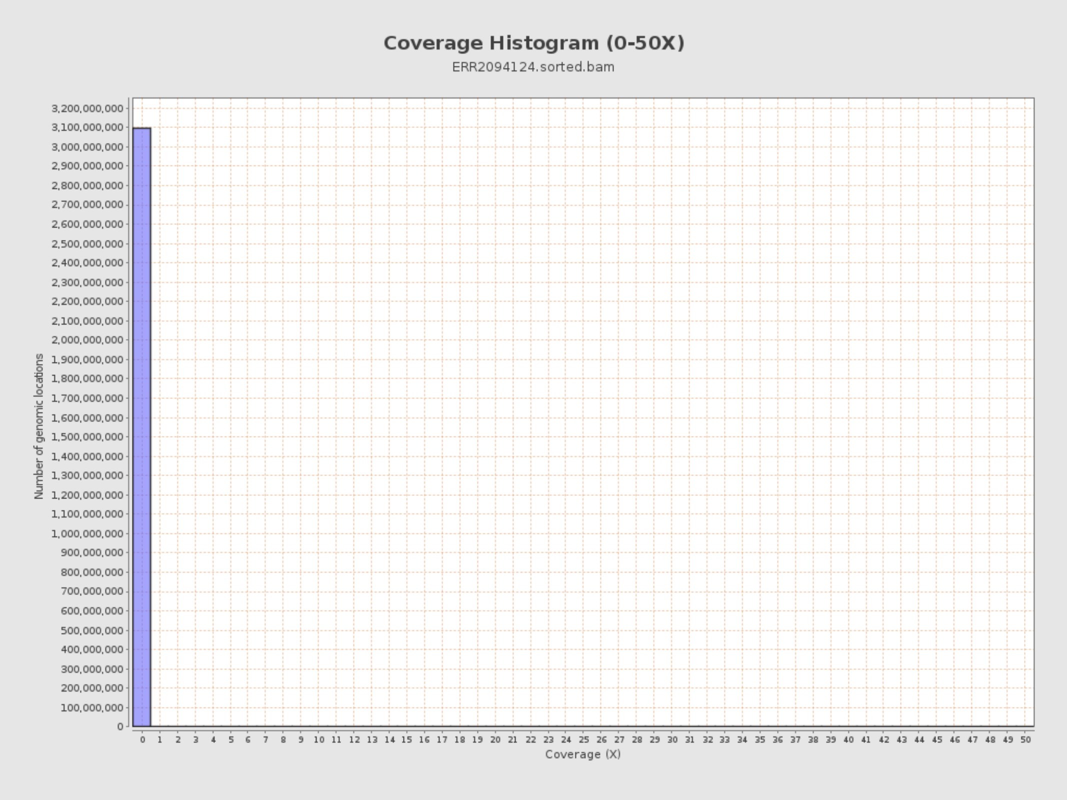
3. Results : Coverage across reference



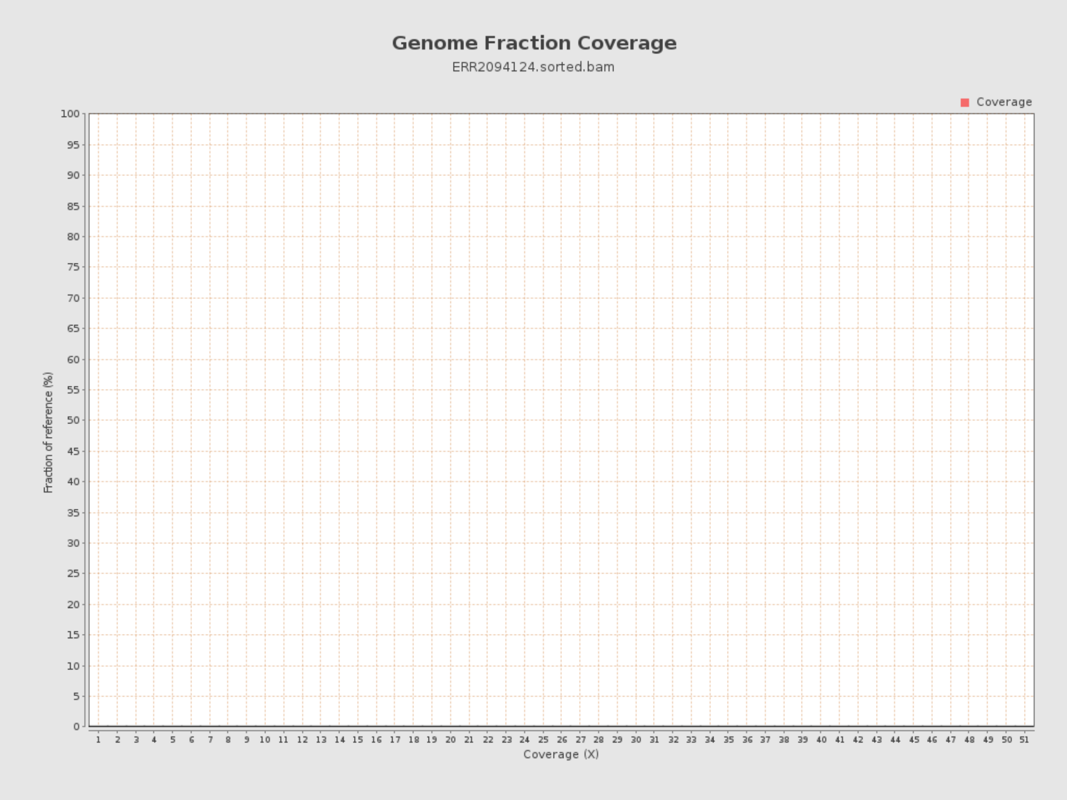
4. Results : Coverage Histogram



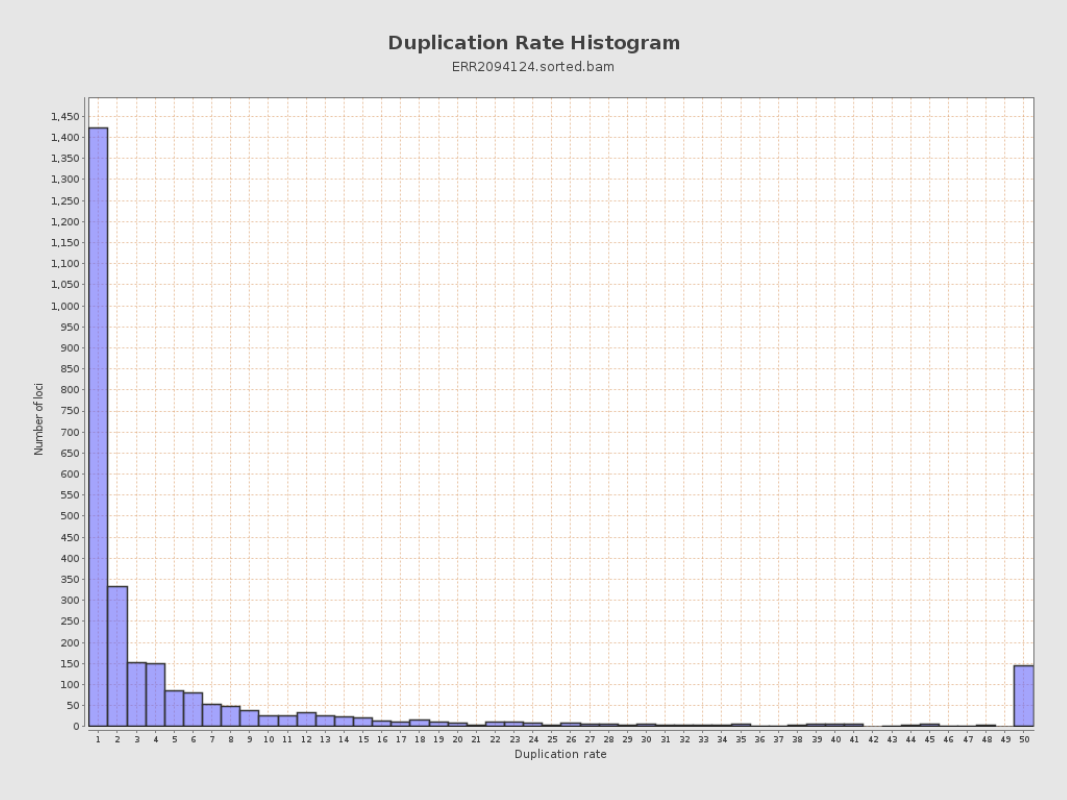
5. Results : Coverage Histogram (0-50X)



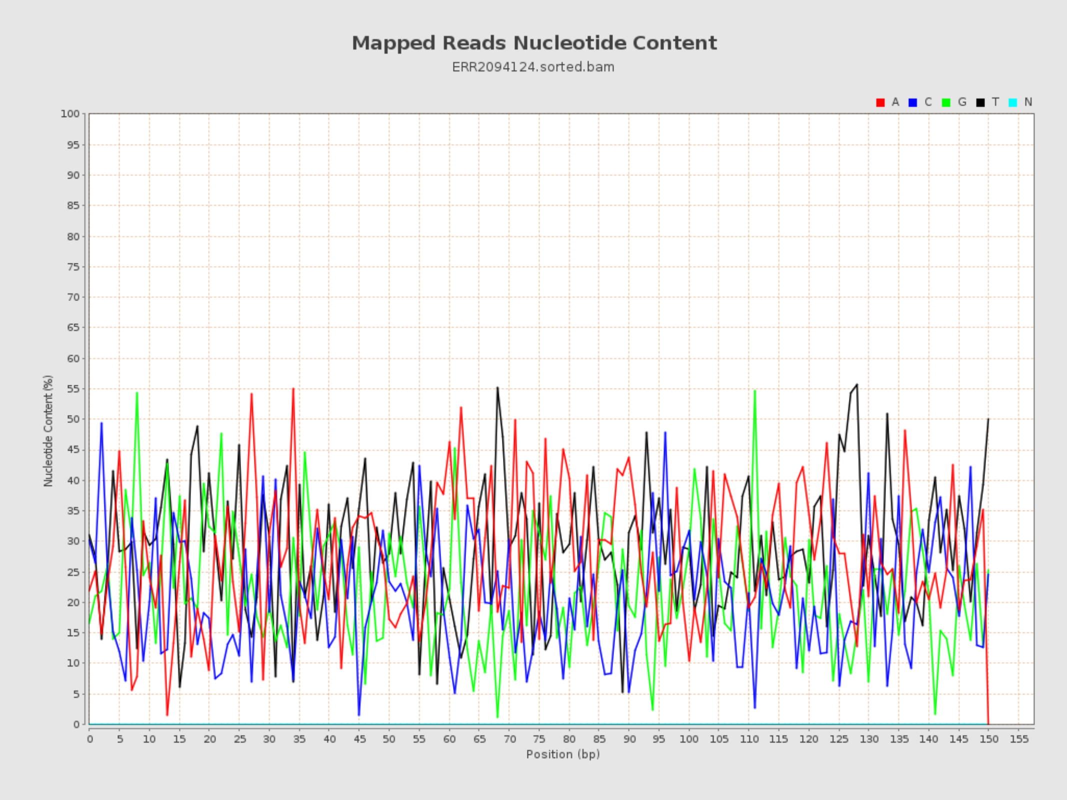
6. Results : Genome Fraction Coverage



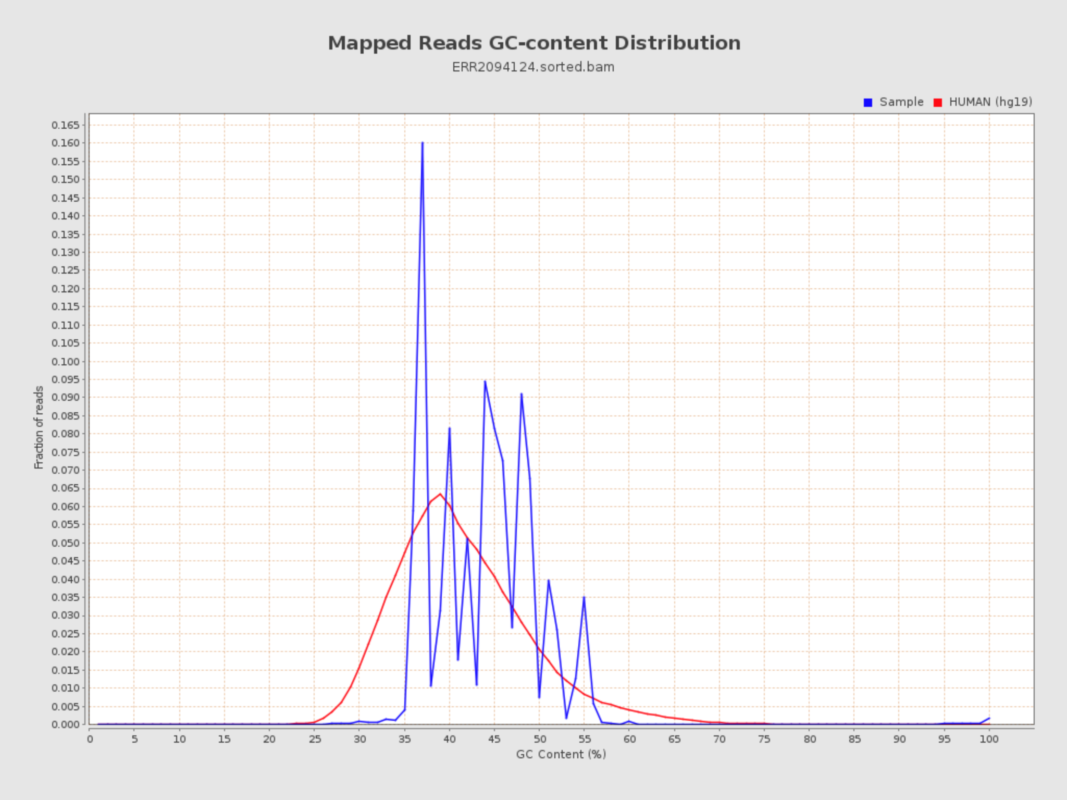
7. Results : Duplication Rate Histogram



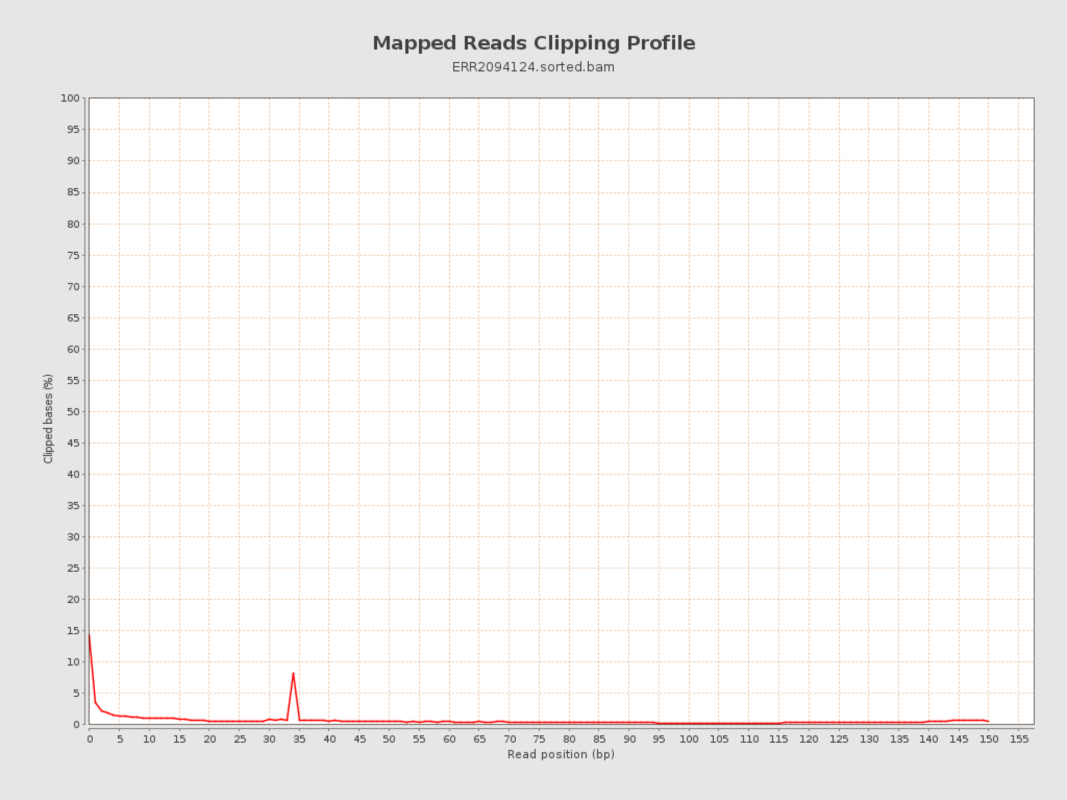
8. Results : Mapped Reads Nucleotide Content



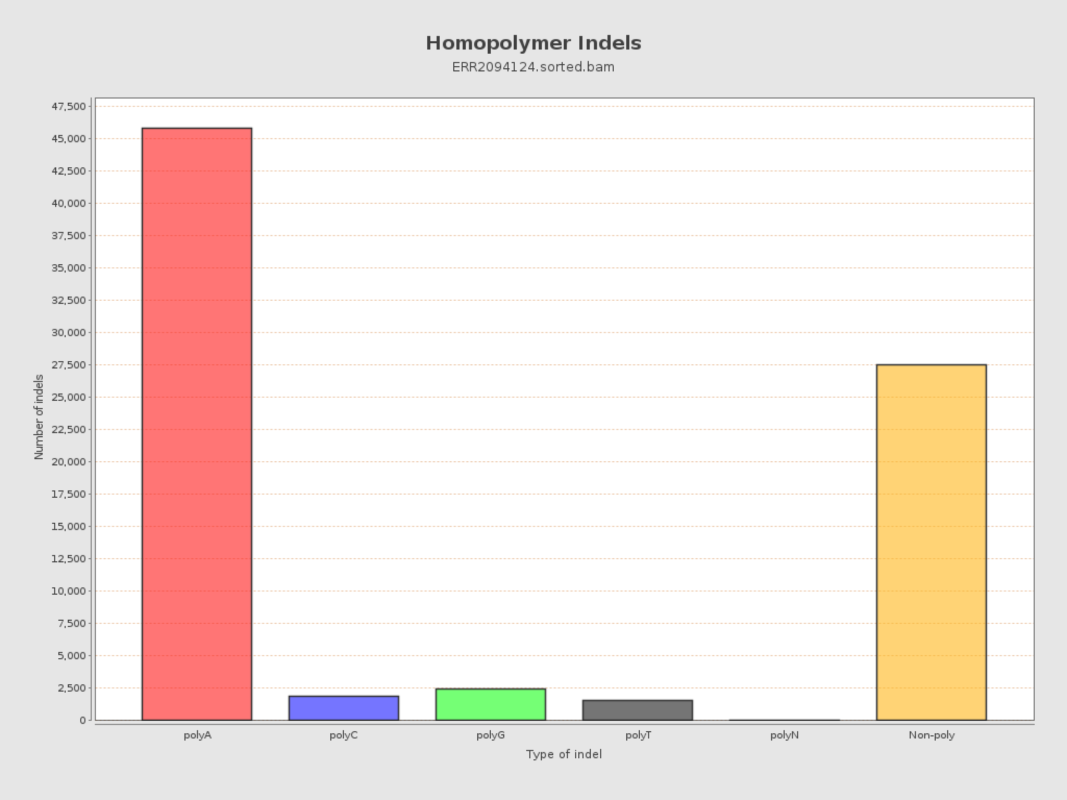
9. Results : Mapped Reads GC-content Distribution



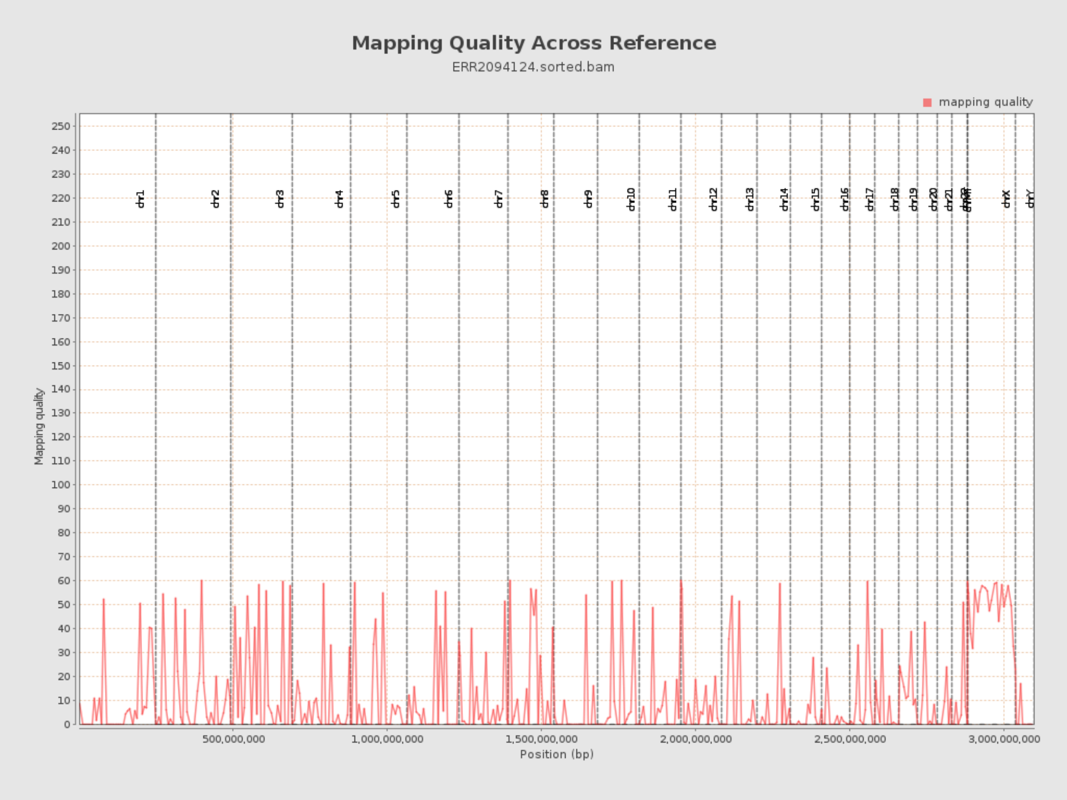
10. Results : Mapped Reads Clipping Profile



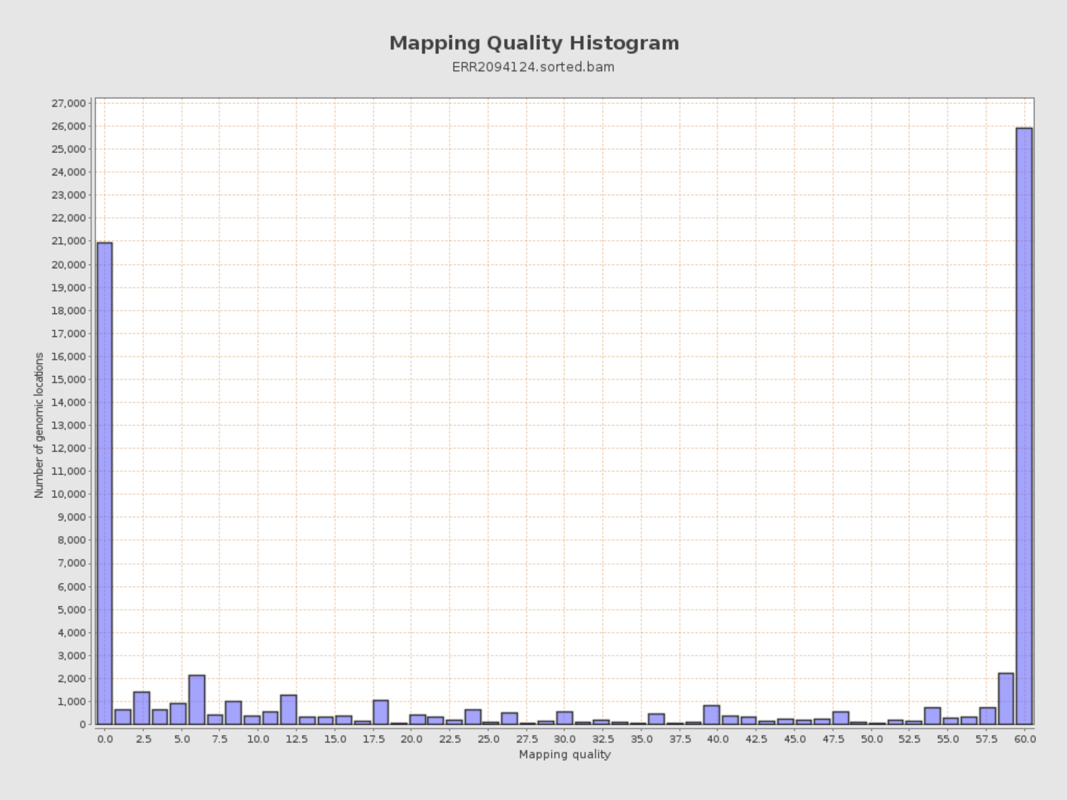
11. Results : Homopolymer Indels



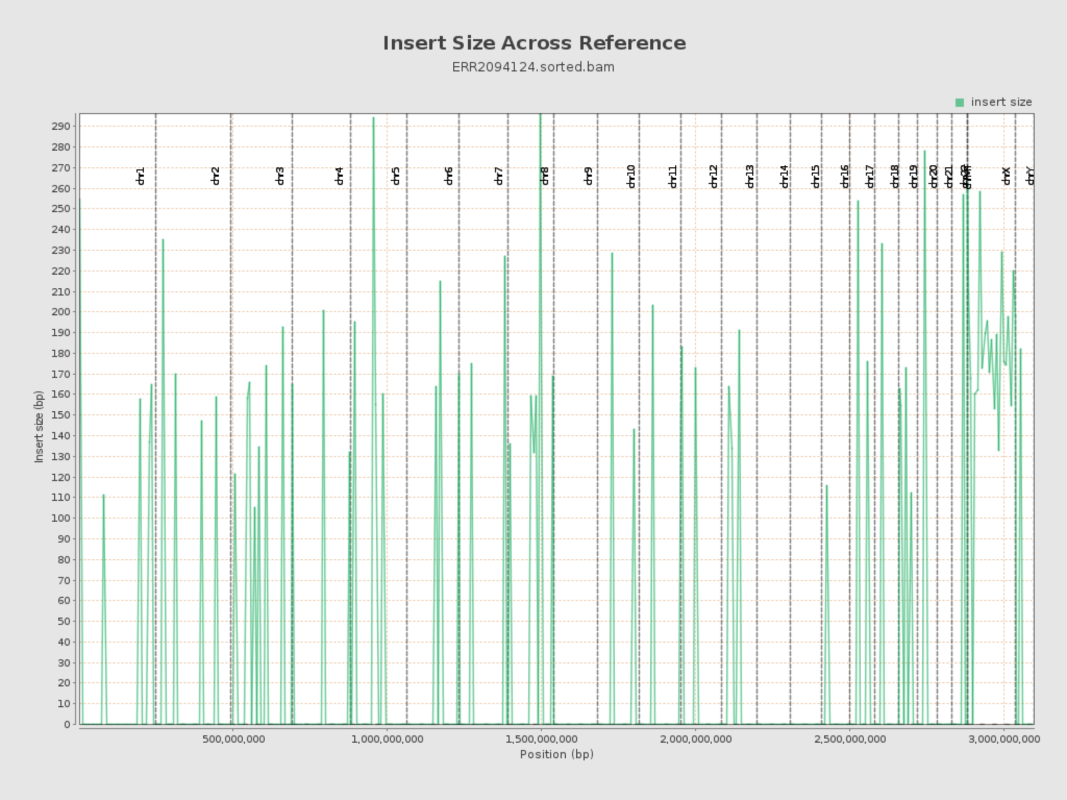
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram